

SEQUENCE LISTING

<110> Brettman, Lee R.
Fox, Judith A.
Allison, David Edward

<120> Method of Administering an Antibody

<130> 1855.2007-001

<140> US 09/748,960
<141> 2000-12-27

<150> US 09/550,082
<151> 2000-04-14

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 396
<212> DNA
<213> *Mus musculus*

<220>
<221> CDS
<222> (1) . . . (396)

<400> 1
atg aag ttg cct gtt agg ctg ttg gtg ctt ctg ttg ttc tgg att cct 48
Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Leu Phe Trp Ile Pro
1 5 10 15

```

ggt tcc gga ggt gat gtt gtg gtg act caa act cca ctc tcc ctg cct 96
Val Ser Gly Gly Asp Val Val Val Thr Gln Thr Pro Leu Ser Leu Pro
          20          25          30

```

gtc agc ttt gga gat caa gtt tct atc tct tgc agg tct agt cag agt 144
Val Ser Phe Gly Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser
35 40 45

```

cct gca aag agt tat ggg aac acc tat ttg tct tgg tac ctg cac aag 192
Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu His Lys
      50          55          60

```

```

cct ggc cag tct cca cag ctc ctc atc tat ggg att tcc aac aga ttt 240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe
 65           70           75           80

```

tct ggg gtg cca gac agg ttc agt ggc agt ggt tca ggg aca gat ttc 288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

```

aca ctc aag atc agc aca ata aag cct gag gac ttg gga atg tat tac 336
Thr Leu Lys Ile Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr
100          105          110

```

| | |
|---|-----|
| tgc tta caa ggt aca cat cag ccg tac acg ttc gga ggg ggg acc aag | 384 |
| Cys Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly Gly Thr Lys | |
| 115 | 120 |
| | 125 |

| | |
|-----------------|-----|
| ctg gaa ata aaa | 396 |
| Leu Glu Ile Lys | |
| 130 | |

<210> 2
 <211> 132
 <212> PRT
 <213> *Mus musculus*

<220>
 <221> SIGNAL
 <222> (1)...(20)
 <223> signal peptide

<221> SITE
 <222> (21)...(43)
 <223> framework 1

<221> SITE
 <222> (44)...(59)
 <223> CDR1

<221> SITE
 <222> (60)...(74)
 <223> framework 2

<221> SITE
 <222> (75)...(81)
 <223> CDR2

<221> SITE
 <222> (82)...(113)
 <223> framework 3

<221> SITE
 <222> (114)...(122)
 <223> CDR3

<221> SITE
 <222> (123)...(132)
 <223> framework 4

<400> 2
 Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Leu Phe Trp Ile Pro
 1 5 10 15
 Val Ser Gly Gly Asp Val Val Val Thr Gln Thr Pro Leu Ser Leu Pro
 20 25 30
 Val Ser Phe Gly Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser
 35 40 45
 Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu His Lys
 50 55 60
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe
 65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe
 85 90 95
 Thr Leu Lys Ile Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr
 100 105 110
 Cys Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly Gly Thr Lys
 115 120 125
 Leu Glu Ile Lys
 130

<210> 3
 <211> 420
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1) ... (420)

<400> 3
 atg gga tgg agc tgt atc atc ctc ttc ttg gta tca aca gct aca agt 48
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ser Thr Ala Thr Ser
 1 5 10 15

gtc cac tcc cag gtc caa ctg cag cag cct ggg gct gag ctt gtg aag 96
 Val His Ser Gln Val Gln Leu Gln Pro Gly Ala Glu Leu Val Lys
 20 25 30

cct ggg act tca gtg aag ctg tcc tgc aag ggt tat ggc tac acc ttc 144
 Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly Tyr Gly Tyr Thr Phe
 35 40 45

acc agc tac tgg atg cac tgg gtg aag cag agg cct gga caa ggc ctt 192
 Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60

gag tgg atc gga gag att gat cct tct gag agt aat act aac tac aat 240
 Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
 65 70 75 80

caa aaa ttc aag ggc aag gcc aca ttg act gta gac att tcc tcc agc 288
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser
 85 90 95

aca gcc tac atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc 336
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

tac tat tgt gca aga ggg ggt tac gac gga tgg gac tat gct att gac 384
 Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
 115 120 125

tac tgg ggt caa ggc acc tca gtc acc gtc tcc tca 420
 Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 130 135 140

<210> 4
 <211> 140

<212> PRT
 <213> Mus musculus

 <220>
 <221> SIGNAL
 <222> (1)...(19)
 <223> signal peptide

 <221> SITE
 <222> (20)...(49)
 <223> framework 1

 <221> SITE
 <222> (50)...(54)
 <223> CDR1

 <221> SITE
 <222> (55)...(68)
 <223> framework 2

 <221> SITE
 <222> (69)...(85)
 <223> CDR2

 <221> SITE
 <222> (86)...(117)
 <223> framework 3

 <221> SITE
 <222> (118)...(129)
 <223> CDR3

 <221> SITE
 <222> (130)...(140)
 <223> framework 4

 <400> 4
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ser Thr Ala Thr Ser
 1 5 10 15
 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 20 25 30
 Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly Tyr Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60
 Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser
 85 90 95
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
 115 120 125
 Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 130 135 140

<210> 5
 <211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Portion of the heavy chain of LDP-02 with a heavy chain signal peptide

<221> CDS

<222> (1) . . . (540)

<400> 5

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atg aaa tgc acc tgg gtc att ctc ttc ttg gta tca aca gct aca agt 48
Met Lys Cys Thr Trp Val Ile Leu Phe Leu Val Ser Thr Ala Thr Ser
   1          5          10          15

```

```

gtc cac tcc cag gtc caa cta gtg cag tct ggg gct gag gtt aag aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
          20          25          30

```

```

cct ggg gct tca gtg aag gtg tcc tgc aag ggt tct ggc tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe
35          40          45

```

```

acc agc tac tgg atg cat tgg gtg agg cag gcg cct ggc caa cgt cta 192
Thr Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu
      50          55          60

```

```

gag tgg atc gga gag att gat cct tct gag agt aat act aac tac aat 240
Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
   65           70           75           80

```

```

caa aaa ttc aag gga cgc gtc aca ttg act gta gac att tcc gct agc 288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Ile Ser Ala Ser
          85           90           95

```

```

aca gcc tac atg gag ctc agc agc ctg aga tct gag gac act gcg gtc 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100          105          110

```

```

tac tat tgt gca aga ggg ggt tac gac gga tgg gac tat gct att gac 384
Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
115           120           125

```

```

tac tgg ggt caa ggc acc ctg gtc acc gtc tcc tca gcc tcc acc aag 432
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130          135          140

```

```

ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg 480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145      150      .      155      .      160

```

```
ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg 528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165          170          175
```

gtg acg gtg tcg 540
Val Thr Val Ser
180

<210> 6
 <211> 180
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Portion of the heavy chain of LDP-02 with a heavy chain signal peptide

<221> SITE
 <222> (19)...(20)
 <223> signal peptide cleavage site

<400> 6
 Met Lys Cys Thr Trp Val Ile Leu Phe Leu Val Ser Thr Ala Thr Ser
 1 5 10 15
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu
 50 55 60
 Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Ile Ser Ala Ser
 85 90 95
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
 115 120 125
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 130 135 140
 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 145 150 155 160
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 165 170 175
 Val Thr Val Ser
 180

<210> 7
 <211> 413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Portion of the light chain LDP-02 with a light chain signal peptide

<221> CDS
 <222> (1)...(413)

<400> 7
 atgaagttgc ctgttaggct gttggtgctt ctgttgttct ggattcctgt ttccggaggt 60
 gatgttgtga tgactcaaag tccactctcc ctgcctgtca cccctggaga accagcttct 120
 atctcttgca ggtctagtca gagtcttgca aagagttatg ggaacaccta tttgtcttgg 180
 tacctgcaga agcctggcca gtctccacag ctcctcatct atgggatttc caacagattt 240
 tctgggggtgc cagacagggtt cagtggcagt ggttcaggga cagatttcac actcaagatc 300
 tcgcgagtag aggctgagga cgtgggagtg tattactgct tacaaggatc acatcagccg 360

tacacgttcg gacaggggac caaggtggaa ataaaacggg ctgatgcggc gcc 413

<210> 8
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Portion of the light chain of LDP-02 with a light chain signal peptide

<221> SITE
 <222> (20)...(21)
 <223> signal peptide cleavage site

<400> 8
 Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Leu Phe Trp Ile Pro
 1 5 10 15
 Val Ser Gly Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
 20 25 30
 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 35 40 45
 Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys
 50 55 60
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe
 65 70 75 80
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 85 90 95
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 100 105 110
 Cys Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 115 120 125
 Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
 130 135

<210> 9
 <211> 16
 <212> PRT
 <213> Mus musculus

<220>
 <221> SITE
 <222> (1)...(16)
 <223> CDR1 of the light chain of antibodies Act-1 and LDP-02

<400> 9
 Arg Ser Ser Gln Ser Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser
 1 5 10 15

<210> 10
 <211> 7
 <212> PRT
 <213> Mus musculus

<220>
 <221> SITE

<222> (1)...(7)
<223> CDR2 of the light chain of antibodies Act-1 and
LDP-02

<400> 10
Gly Ile Ser Asn Arg Phe Ser
1 5

<210> 11
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> SITE
<222> (1)...(9)
<223> CDR3 of the light chain of antibodies Act-1 and
LDP-02

<400> 11
Leu Gln Gly Thr His Gln Pro Tyr Thr
1 5

<210> 12
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> SITE
<222> (1)...(5)
<223> CDR1 of the heavy chain of antibodies Act-1 and
LDP-02

<400> 12
Ser Tyr Trp Met His
1 5

<210> 13
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> SITE
<222> (1)...(17)
<223> CDR2 of the heavy chain of antibodies Act-1 and
LDP-02

<400> 13
Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15
Gly

<210> 14
 <211> 12
 <212> PRT
 <213> Mus musculus

<220>
 <221> SITE
 <222> (1)...(12)
 <223> CDR3 of the heavy chain of antibodies Act-1 and
 LDP-02

<400> 14
 Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp Tyr
 1 5 10

<210> 15
 <211> 396
 <212> DNA
 <213> Mus musculus

<400> 15
 ttttatttcc agtttgttcc cccctccgaa cgtgtacggc tgatgtgtac cttgttaagca 60
 gtaatacatt cccaaatgcct caggctttat tggctgtatc ttggatgtgtga aatctgtccc 120
 tgaaccactg ccactgaacc tggctggcac cccagaaaaat ctgttggaaa tcccatagat 180
 gagggagctgt ggagactggc caggcttggc caggtaccaa gacaaaatagg tgttccatata 240
 actctttgca agactctgac tagacactgca agagatagaa acttgatctc caaaagctgac 300
 aggccaggag agtggagttt gagtcaccac aacatcacct ccggaaacacag gaatccagaa 360
 caacagaagc accaacagcc taacaggcaa cttcat 396

<210> 16
 <211> 420
 <212> DNA
 <213> Mus musculus

<400> 16
 tgaggagacg gtgactgagg tgccttgacc ccagtagtca atagcatagt cccatccgtc 60
 gtaacccctt cttgcacaat agtagaccgc agagtcctca gatgtcaggc tgctgagctg 120
 catgttaggt gtgctggagg aaatgtctac agtcaatgtg gcttgcctt tgaatttttg 180
 attgttagttt gtattactct cagaaggatc aatctctccg atccactcaa ggccttgc 240
 aggccctctgc ttcacccagt gcatccagta gctggtaag gtgttagccat aacccttgca 300
 ggacagcttc actgaagtcc caggcttcac aagctcagcc ccaggctgtgt gcagttggac 360
 ctgggagtgg acactttagt ctgttatac caagaagagg atgatacagc tccatccat 420